

F3 3. A primer design system according to claim 2, said selection conditions include at least one of a predetermined base length, a range of GC content and a range of Tm.

F4 4. A primer design system according to claim 1, further comprising means for evaluating specificity of each designed primer or primer pair.

FS SUB G2 30. A method for designing primers, comprising the steps of:  
selecting at least one DNA nucleotide sequence from a genomic DNA database;  
predicting a plurality of exons of said selected DNA nucleotide;  
simultaneously designing a plurality of primer pairs by using each of the predicted exons as a template; and  
automatically collating said plurality of primer pairs with said predicted exons and the DNA nucleotide sequence.

31. A method for designing primers according to claim 30, further comprising a step of selecting a plurality of primer pairs meeting certain selection conditions from said plurality of designed primer pairs, wherein said extraction conditions include at least one of a predetermined base length, a GC content, Tm.

32. A method for designing primers according to claim 30, further comprising a step of evaluating specificity of each designed primer or primer pair.

Please add new claims as follows:

FL 33. A primer design system according to claim 1, further comprising randomly dividing fragments of a genomic DNA as templates for exon prediction.

SUB G3 34. A primer design system, comprising:  
means for selecting at least one genomic DNA nucleotide sequence from a database including a plurality of DNA nucleotide sequences;  
means for predicting a plurality of exons of said selected DNA nucleotide and for storing positions of the predicted exons;  
means for designing a plurality of primer pairs by using each of the predicted exons as a template; and  
means for evaluating specificity of each designed primer or each designed primer pair.

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35. A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer by conducting BLAST searches for a full sequence of the primer via at least one repeat database and at least one genome database.
36. A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer by conducting a BLAST search for any undesirable sequence contained therein.
37. A primer design system according to claim 34, wherein the means for evaluating specificity evaluates each designed primer pair by conducting justification checks on each multiplication region in the DNA which contains an exact sequence as the primer but positioned elsewhere on the DNA.

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